Genome Institute of Singapore
A*STAR GIS

THE GIS
SPEAKER SERIES

3D genome folding and transcription regulation

Dr. Yijun Ruan
Professor, Zhejiang University

Host: Wan Yue

Friday 28 November 2025
4.00pm – 4.45pm

GIS L2 – Breakout Area
60 Biopolis Street, Genome, Singapore 138672

About The Speaker

Dr. Yijun Ruan is Qiusi Endowed Chair Professor at Zhejiang University, Chief Investigator at the Institute of Life Sciences, and the inaugural Director of the 3D Genomics Committee of the Chinese Society of Genetics. His primary research focuses on exploring the causal relationship between the 3D structure of the human genomes and the regulatory function of gene transcription. He has published over 160 research articles, including numerous high-impact papers in Cell, Nature, and Science. Professor Ruan graduated from Huazhong Agricultural University and earned his Ph.D. in Molecular Biology from the University of Maryland. After experienced in biotech industry, he joined Genome Institute of Singapore (GIS) as a sr. group leader in 2002, and later moved to The Jackson Laboratory and University of Connecticut as the Florine Deschenes Roux Endowed Chair Professor in 2012-2022. Dr. Ruan received numerous honours, including the prestigious National Science Award in Singapore in 2006. He is widely recognized as a pioneer in developing applications of NGS, a founder of 3D genome biology, and played pivotal roles in major international projects such as ENCODE and 4DN. His team is currently advancing 3D genomics into diverse biomedical questions at single-cell/single-molecule levels.

About The Seminar

Exploring the genomic basis of transcriptional programs has been a longstanding research focus. However, the causal relationship of the genomic structure and the functional output of gene expression in vivo is still elusive, and bulk-cell based multi-omic analyses are not adequate to address this challenge. To this direction, we have developed single-molecule (ChIA-Drop) and single-cell multi-omic (ChAIR) approaches to decipher the relationship of chromatin folding as a structural basis and gene transcription as a functional output. Specifically, we investigated the interplays between CTCF, cohesin, and RNAPII in human cells and revealed that only the long-range chromatin loops between distal (super-)enhancers and promoters of cell-type-specific genes are cohesin-dependent, while most constitutive genes display short-range transcription loops and are largely cohesin-independent. Our results uncovered new mechanistic insights of cohesin's multi-functions in chromatin looping and transcription regulation.